SBI3U

**Cladograms (Phylogenetic Trees)**

We know how to determine evolutionary relationships by looking at phylogenetic trees (cladograms).

Cladograms are constructed based on the presence or absence of recently evolved traits (“derived traits”) in a group of organisms. Tutorial 1 (page 351) shows how to construct a cladogram from a table of *shared* derived characteristics (synapomorphies).

You are expected to be able to construct the cladogram from a table of synapomorphies, such as Table 2 on page 351.

Steps:

1. The “outgroup” is the species/group that is not closely related to the other species/groups. Choose

the outgroup based on the least number of shared characteristics. Draw a “V” with the outgroup

at the upper left. The base of the “V” represents the common ancestor of all the species.

2. Then look at the other shared traits & determine which trait likely evolved next (i.e. the one that

the greatest number of species/groups left share), and add another branch. Label the shared

traits on the cladogram. See Figure 7 (page 352) for an example, and the steps in more detail.

Try Question #111 on page 388. Draw your cladogram below:

Draw a cladogram based on this table of shared derived traits below:

